

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2003, 13:48:12 ; Search time 0.001 Seconds
(without alignments)
178.084 Million cell updates/sec

Title: us-09-869-540a-11

Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGGSS.....LRVSNQTADEERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 422 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-09-478-601-2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2207	99.8	422	1	us-09-478-601-2

ALIGNMENTS

RESULT 1
us-09-478-601-2

Query Match 99.8% ; Score 2207 ; DB 1 ; Length 422 ;
Best Local Similarity 99.8% ; Pred. No. 0 ;
Matches 421 ; Conservative 1 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY	1	MSVGAMKKGVGRAVGLGGSSCCATTEEDPLPNCGACAPGGGRRRLPPAWEGSSARL 60
DB	1	MSVGAMKKGVGRAVGLGGSSCCATTEEDPLPDCGACAPGGGRRRLPPAWEGSSARL 60
QY	61	WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISIYINIMPSVFTIC 120
DB	61	WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISIYINIMPSVFTIC 120
QY	121	LLGIGNSTYIFAVVKKSKLHKCNVDFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
DB	121	LLGIGNSTYIFAVVKKSKLHKCNVDFIINLSVVDLLFLGMPFMIHQLMNGVWHF 180
QY	181	GETMCTLTAMDANSOFTSTYIILTAMADRYLATVHPISSTKRPASVATLYCLMAL 240
DB	181	GETMCTLTAMDANSOFTSTYIILTAMADRYLATVHPISSTKRPASVATLYCLMAL 240
QY	241	FISITPVMLYARLIPPGGAVGCGIRLPNDTDLVFTLYOFLAFALPFWVITAAVRI 300
DB	241	FISITPVMLYARLIPPGGAVGCGIRLPNDTDLVFTLYOFLAFALPFWVITAAVRI 300

QY	301	LQRTSSVAPASORSIRLRTKRYRTAATCIVFVCGAPYYVLTQLTQLSISRPFTLFVY 360
DB	301	LQRTSSVAPASORSIRLRTKRYRTAATCIVFVCGAPYYVLTQLTQLSISRPFTLFVY 360
QY	361	LYNAISLGYANSCLNPFYIIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESK 420
DB	361	LYNAISLGYANSCLNPFYIIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESK 420
QY	421	GT 422
DB	421	GT 422

Search completed: July 7, 2003, 13:48:13
Job time : 1 sec

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OM protein - protein search, using sw model

Run on: July 7, 2003, 13:42:55 ; Search time 0.001 Seconds
(without alignments)
148.966 Million cell updates/sec

Title: us-09-869-540a-11

Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGGG.....LRAVSNQTADEERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 353 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-09-925-776-2 *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1824	82.5	353	1	us-09-925-776-2

ALIGNMENTS

RESULT 1
us-09-925-776-2

Query Match 82.5% ; Score 1824 ; DB 1 ; Length 353 ;
Best Local Similarity 100.0% ; Pred. No. 0 ;
Matches 353 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY	70	MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIIMPVFGTICLLGIGNST	129
DB	1	MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIIMPVFGTICLLGIGNST	60
QY	130	VIFAVVKKSKLHMCNNPDIIFIINLSYVDLFLGLGMPMTIHLGNGVWHFGETMCTLIT	189
DB	61	VIFAVVKKSKLHMCNNPDIIFIINLSYVDLFLGLGMPMTIHLGNGVWHFGETMCTLIT	120
QY	190	AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWL	249
DB	121	AMDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFISTIPVWL	180
QY	250	YARLIPEPGGAVCGGIRLPNPDLYWFTLYOFFLAFALPFVYITAAVYRIIQRMTSSVA	309
DB	181	YARLIPEPGGAVCGGIRLPNPDLYWFTLYOFFLAFALPFVYITAAVYRIIQRMTSSVA	240
QY	310	PASORSIRLRTKRTVTAICLVFVCAPYVVLQTLQISIRPTLTFFVYLYNNAISLG	369
DB	241	PASORSIRLRTKRTVTAICLVFVCAPYVVLQTLQISIRPTLTFFVYLYNNAISLG	300

QY 370 YANSCINPEYIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 422
DB 301 YANSCINPEYIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 353

Search completed: July 7, 2003, 13:42:55
Job time : 0.001 secs